

**Table S11. *Clostridium innocuum* strain SB23 genome sequencing statistics.**

Total reads	895,654
Assembled reads	862,857
Partial reads	12,846
Singleton reads	2,206
Repeat reads	224
Outlier reads	799
Too short reads	16,722
%reads assembled	96
Number of contigs	53
Number of bases	4,337,003
Avg contig size	81,830
N50 contig size	147,006
Largest contig size	456,585
Q40+ bases	99.98%
Q39- bases	0.02%